



SEQUENCE LISTING

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Metcalf, Donald
Zhang, Jian G.

<120> NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
ENCODING SAME

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<140> 09/688,286

<141> 2000-10-31

<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 1383

<212> DNA

<213> Mus musculus

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<221> CDS

<222> (61) .. (1338)

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Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
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acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca 156
Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Thr Glu Val Gln Pro
20 25 30

cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204
Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
35 40 45

tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252
Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
50 55 60

tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300
Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
65 70 75 80

act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag 348
Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
85 90 95

gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg 396
Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
100 105 110

gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg 444
Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
115 120 125

act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc 492
Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
130 135 140

tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac 540
Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
145 150 155 160

tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat 588
Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
165 170 175

aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa 636
Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
180 185 190

cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat 684

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gtg	aaa	cct	gat	cct	cca	cat	att	aaa	cat	ctt	ctc	ctc	aaa	aat	ggc	780
Val	Lys	Pro	Asp	Pro	Pro	His	Ile	Lys	His	Leu	Leu	Leu	Lys	Asn	Gly	
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gcc	tta	tta	gtg	cag	tgg	aag	aat	cca	caa	aat	ttt	aga	agc	aga	tgc	828
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Leu	Thr	Tyr	Glu	Val	Glu	Val	Asn	Asn	Thr	Gln	Thr	Asp	Arg	His	Asn	
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att	tta	gag	gtt	gaa	gag	gac	aaa	tgc	cag	aat	tcc	gaa	tct	gat	aga	924
Ile	Leu	Glu	Val	Glu	Glu	Asp	Lys	Cys	Gln	Asn	Ser	Glu	Ser	Asp	Arg	
		275					280					285				
aac	atg	gag	ggt	aca	agt	tgt	ttc	caa	ctc	cct	ggc	gtt	ctt	gcc	gac	972
Asn	Met	Glu	Gly	Thr	Ser	Cys	Phe	Gln	Leu	Pro	Gly	Val	Leu	Ala	Asp	
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Ala	Val	Tyr	Thr	Val	Arg	Val	Arg	Val	Lys	Thr	Asn	Lys	Leu	Cys	Phe	
	305				310				315						320	
gat	gac	aac	aaa	ctg	tgg	agt	gat	tgg	agt	gaa	gca	cag	agt	ata	ggc	1068
Asp	Asp	Asn	Lys	Leu	Trp	Ser	Asp	Trp	Ser	Glu	Ala	Gln	Ser	Ile	Gly	
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aag	gag	caa	aac	tcc	acc	ttc	tac	acc	acc	atg	tta	ctc	acc	att	cca	1116
Lys	Glu	Gln	Asn	Ser	Thr	Phe	Tyr	Thr	Thr	Met	Leu	Leu	Thr	Ile	Pro	
			340					345					350			
gtc	ttt	gtc	gca	gtg	gca	gtc	ata	atc	ctc	ctt	ttt	tac	ctg	aaa	agg	1164
Val	Phe	Val	Ala	Val	Ala	Val	Ile	Ile	Leu	Leu	Phe	Tyr	Leu	Lys	Arg	
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ctt	aag	atc	att	ata	ttt	cct	cca	att	cct	gat	cct	ggc	aag	att	ttt	1212
Leu	Lys	Ile	Ile	Ile	Phe	Pro	Pro	Ile	Pro	Asp	Pro	Gly	Lys	Ile	Phe	
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aaa	gaa	atg	ttt	gga	gac	cag	aat	gat	gat	acc	ctg	cac	tgg	aag	aag	1260
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	385				390					395					400	
tat	gac	atc	tat	gag	aaa	caa	tcc	aaa	gaa	gaa	acg	gat	tct	gta	gtg	1308
Tyr	Asp	Ile	Tyr	Glu	Lys	Gln	Ser	Lys	Glu	Glu	Thr	Asp	Ser	Val	Val	
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ctg	ata	gaa	aac	ctg	aag	aaa	gca	gct	cct	tgatgggggag	aagtgatttc					1358
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1383

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<213> Mus musculus

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<221> unsure

<222> (21)

<223> authors are unsure about the sequence assignment

<220>

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<222> (194)

<223> authors are unsure about the sequence assignment

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20 25 30

Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
35 40 45

Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
50 55 60

Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
65 70 75 80

Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
85 90 95

Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
100 105 110

Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
115 120 125

Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
145 150 155 160

Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
165 170 175

Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
180 185 190

Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
195 200 205

Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr

210

215

220

Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
 225 230 235 240

Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
 245 250 255

Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
 260 265 270

Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
 275 280 285

Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
 290 295 300

Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
 305 310 315 320

Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
 325 330 335

Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
 340 345 350

Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
 355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
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Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
 405 410 415

Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
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<210> 3

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (61) .. (1338)

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Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys

1

5

10

15

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cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata	204
Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile	
35 40 45	
tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg	252
Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp	
50 55 60	
tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa	300
Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu	
65 70 75 80	
act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa	348
Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln	
85 90 95	
gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg	396
Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu	
100 105 110	
gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg	444
Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val	
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act gag ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct	492
Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser	
130 135 140	
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Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr	
145 150 155 160	
tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt	588
Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe	
165 170 175	
aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag	636
Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys	
180 185 190	
gat tcc agt ttt gaa caa cac agt gtc caa ata atg gtc aag gat aat	684
Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn	
195 200 205	
gca gga aaa att aaa cca tcc ttc aat ata gtg cct tta act tcc cgt	732
Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg	
210 215 220	
gtg aaa cct gat cct cca cat att aaa aac ctc tcc ttc cac aat gat	780
Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp	
225 230 235 240	
gac cta tat gtg caa tgg gag aat cca cag aat ttt att agc aga tgc	828

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aat	gtg	gag	aat	aca	tct	tgt	ttc	atg	gtc	cct	ggg	gtt	ctt	cct	gat	972	
Asn	Val	Glu	Asn	Thr	Ser	Cys	Phe	Met	Val	Pro	Gly	Val	Leu	Pro	Asp		
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gtc	atc	gtc	gca	ggg	gca	atc	ata	gta	ctc	ctg	ctt	tac	cta	aaa	agg	1164	
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ctc	aag	att	att	ata	ttc	cct	cca	att	cct	gat	cct	ggc	aag	att	ttt	1212	
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	370					375					380						
aaa	gaa	atg	ttt	gga	gac	cag	aat	gat	gat	act	ctg	cac	tgg	aag	aag	1260	
Lys	Glu	Met	Phe	Gly	Asp	Gln	Asn	Asp	Asp	Thr	Leu	His	Trp	Lys	Lys		
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ctg	ata	gaa	aac	ctg	aag	aaa	gcc	tct	cag	tgatggagat	aattttatttt					1358	
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<211> 426

<212> PRT

<213> Homo sapiens

<400> 4

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 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
 35 40 45
 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
 50 55 60
 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
 65 70 75 80
 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
 85 90 95
 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
 100 105 110
 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 115 120 125
 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
 130 135 140
 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
 145 150 155 160
 Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
 165 170 175
 Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys
 180 185 190
 Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn
 195 200 205
 Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg
 210 215 220
 Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp
 225 230 235 240
 Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys
 245 250 255
 Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn
 260 265 270
 Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg
 275 280 285
 Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp
 290 295 300
 Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr
 305 310 315 320
 Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly

325

330

335

Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
 340 345 350

Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
 355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
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Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val
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<210> 5

<211> 30

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: signal sequence of murine IL-3

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Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser
 20 25 30

<210> 6

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: N-terminal FLAG epitope-tag

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Asp Tyr Lys Asp Asp Asp Asp Lys
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<210> 7

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo 1478 5'

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agcttctaga acagaagttc agccacctgt g

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<210> 8
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aactccacct tctacaccac ctgatctaga

30

<210> 9
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<212> PRT
<213> Unknown

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<223> Description of Unknown Organism:NR4 Motif

<220>
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<222> (3)
<223> Xaa may be any amino acid

<400> 9
Trp Ser Xaa Trp Ser
1 5

<210> 10
<211> 27
<212> PRT
<213> Unknown

<220>
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of mNR4 (major)

<220>
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<222> (24)
<223> Xaa may be any amino acid

<400> 10

Asp Tyr Lys Asp Asp Asp Asp Tyr Lys Asp Asp Asp Glu Ser Arg Thr Glu
1 5 10 15

Val Gln Pro Pro Val Thr Xaa Leu Ser Val
20 25

<210> 11
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of mNR4 (minor)

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<222> (24)
<223> Xaa may be any amino acid

<400> 11

Ala Ser Ile Ser Ser Ser Asp Tyr Lys Asp Asp Asp Glu Ser Arg Thr Glu
1 5 10 15

Val Gln Pro Pro Val Thr Xaa Leu Ser Val
20 25

<210> 12
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide motif found in
many members of the haemopoietin receptor family

<400> 12

Trp Ser Asp Trp Ser
1 5